

R. Hutsuk

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/467,100

DATE: 04/14/2000
TIME: 06:39:35

INPUT SET: S35296.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
2

3 (1) General Information:

4 (i) APPLICANT: Coleman, Roger
5 Stuart, Susan G.

6 (ii) TITLE OF INVENTION: A NOVEL HUMAN JAK2 KINASE

7 (iii) NUMBER OF SEQUENCES: 5

8 (iv) CORRESPONDENCE ADDRESS:

9 (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
10 (B) STREET: 3174 Porter Drive
11 (C) CITY: Palo Alto
12 (D) STATE: CA
13 (E) COUNTRY: US
14 (F) ZIP: 94304

15 (v) COMPUTER READABLE FORM:

16 (A) MEDIUM TYPE: Diskette
17 (B) COMPUTER: IBM Compatible
18 (C) OPERATING SYSTEM: DOS
19 (D) SOFTWARE: FastSEQ Version 1.5

20 (vi) CURRENT APPLICATION DATA:

21 (A) APPLICATION NUMBER: 09/467,100
22 (B) FILING DATE:
23 (C) CLASSIFICATION:

24 (vii) PRIOR APPLICATION DATA:

25 (A) APPLICATION NUMBER: US/08/567,508
26 (B) FILING DATE: 05-DEC-1995

27 (viii) ATTORNEY/AGENT INFORMATION:

28 (A) NAME: Billings, Lucy J.
29 (B) REGISTRATION NUMBER: 36,749
30 (C) REFERENCE/DOCKET NUMBER: PF-0049US

31 (ix) TELECOMMUNICATION INFORMATION:

32 (A) TELEPHONE: 650-855-0555
33 (B) TELEFAX: 650-845-4166

34 (2) INFORMATION FOR SEQ ID NO:1:

35 ENTERED

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47 (i) SEQUENCE CHARACTERISTICS:
 48 (A) LENGTH: 4482 base pairs
 49 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: single
 51 (D) TOPOLOGY: linear
 52

53 (ii) MOLECULE TYPE: cDNA
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55 (vii) IMMEDIATE SOURCE:
 56 (A) LIBRARY: Placenta
 57 (B) CLONE: 179527
 58

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 60

61 CCACCGTCC	GGTTGCCAAC	CCGCAGGCAG	CTGGCGCTT	CATCCCACCC	TCACCCCTTT	60
62 CCAGCCAAGG	TGGCTGATCG	GAGTCAGGCT	CTCGAGGTG	CATTGCCACG	AAACGGNGTG	120
63 TGTGAGCGCG	TTGTCCCCGG	NCCCCGGGGC	CACTTCCCCT	CGGCCTAGNA	GACTGGACTG	180
64 GGGAGGACG	GGTCTGTTGT	ACCCGGGAGG	TGGAAGGAAA	AGCCGAAAGC	GGAGAAAGTGT	240
65 GCGGGAGGGG	AGTCTCCGCG	CGGAGGNAGA	CCGGNCTCCT	CCAGTGCAGG	TTGTGCGCTG	300:
66 GGGAGCCAGC	CASGGCAAAT	GTTCCTGAAA	AGACTCTGCA	TGGGAATGGC	CTGCCTTACG	360
67 ATGACAGAAA	TGGAGGAAAC	ATCCACCTCT	TCTATATATC	AGAATGGTGA	TATTTCTGGA	420
68 AATGCCAATT	CTATGAAGCA	AATAGATCCA	GTTCTTCAGG	TGTATCTTTA	CCATTCCCTT	480
69 GGGAAATCTG	AGGCAGATTA	TCTGACCTTT	CCATCTGGGG	AGTATGTTGG	AGAAGAAATC	540
70 TGTATTGCTG	CTTCTAAAGC	TTGTGGTATC	ACACCTGTGT	ATCATAATAT	GTTTGCTTTA	600
71 ATGAGTGAAA	CAGAAAGGAT	CTGGTATCCA	CCCAACCATG	TCTTCCATAT	AGATGAGTCA	660
72 ACCAGGCATA	ATGTACTCTA	CAGAATAAGA	TTTTACTTTC	CTCGTTGGTA	TTGCAGTGGC	720
73 AGCAACAGAG	CCTATCGGCA	TGGAATATCT	CGAGGTGCTG	AAGCTCCTCT	TCTTGATGAC	780
74 TTTGTCATGT	CTTACCTCTT	TGCTCAGTGG	CGGCATGATT	TTGTGCATGG	ATGGATAAAA	840
75 GTACCTGTGA	CTCATGAAAC	ACAGGAAGAA	TGTCTGGGA	TGACAGTGT	AGATATGATG	900
76 AGAATAGCCA	AAGAAAACGA	TCAAACCCCCA	CTGGCCATCT	ATAACTCTAT	CAGCTACAAG	960
77 ACATTCTTAC	CACAATGTAT	TCGAGCAAAG	ATCCAAGACT	ATCATATTTT	GACAAGGAAG	1020
78 CGAATAAGGT	ACAGATTTCG	CAGATTATT	CAGCAATTCA	GCCAATGCAA	AGCCACTGCC	1080
79 AGAAACTTGA	AACTTAAGTA	TCTTATAAAT	CTGGAAACTC	TGCACTCTGC	CTTCTACACA	1140
80 GAGAAATTTG	AAGTAAAAGA	ACCTGGAAGT	GGTCCTTCAG	GTGAGGAGAT	TTTGCAACC	1200
81 ATTATAATAA	CTGGAAACGG	TGGAATTCA	TGGTCAAGAG	GGAAACATAA	AGAAAGTGAG	1260
82 ACACTGACAG	AACAGGATTT	ACAGTTATAT	TGCGATTTC	CTAATATTAT	TGATGTCAGT	1320
83 ATTAAGCAAG	CAAACCAAGA	GGGTTCAAAT	GAAAGCCGAG	TTGTAACAT	CCATAAGCAA	1380
84 GATGGTAAAA	ATCTGGAAAT	TGAACCTAGC	TCATTAAGGG	AAGCTTTGTC	TTTCGTGTCA	1440
85 TTAATTGATG	GATATTATAG	ATTAACCTGCA	GATGCACATC	ATTACCTCTG	AAAGAAGTA	1500
86 GCACCTCCAG	CCGTGCTTGA	AAATATACAA	AGCAACTGTC	ATGGCCAAT	TTCGATGGAT	1560
87 TTTGCCATTA	GTAAACTGAA	GAAAGCAGGT	AATCAGACTG	GAATGTATGT	ACTTCGATGC	1620
88 AGTCCTAAGG	ACTTTAATAA	ATATTTTTG	ACTTTGCTG	TCGAGCGAGA	AAATGTCATT	1680
89 GAATATAAAC	ACTGTTGAT	TACAAAAAAAT	GAGAATGAAG	AGTACAACCT	CAGTGGGACA	1740
90 AAGAAGAACT	TCAGCAGTCT	AAAAGATCTT	TTGAATTGTT	ACCAGATGGA	AACTGTTCGC	1800
91 TCAGACAATA	TAATTTCCA	GTTCCTAA	TGCTGTCCCC	CAAAGCCAAA	AGATAAAATCA	1860
92 AACCTTCTAG	TCTTCAGAAC	GAATGGTGT	TCTGATGTAC	CAACCTCACC	AACATTACAG	1920
93 AGGCCTACTC	ATATGAACCA	AATGGTGT	CACAAATCA	GAAATGAAGA	TTTGATATT	1980
94 AATGAAAGCC	TTGGCCAAGG	CACTTTTACA	AAGATTTTA	AAGGCGTACG	AAGAGAAGTA	2040
95 GGAGACTACG	GTCAACTGCA	TGAAACAGAA	GTTCTTTAA	AAGTTCTGGA	AAAGCACAC	2100
96 AGGAACTATT	CAGAGTCTTT	CTTGTAGCA	GCAAGTATGA	TGAGCAAGCT	TTCTCACAAG	2160
97 CATTGGTTT	TAAATTATGG	AGTATGTGTC	TGTGGAGACG	AGAATATTCT	GGTTCAAGGAG	2220
98 TTTGTAAAAT	TTGGATCACT	AGATACATAT	CTGAAAAAGA	ATAAAAATTG	TATAAATATA	2280
99 TTATGGAAAC	TTGAAGTTGC	TAAACAGTTG	GCATGGGCCA	TGCATTTCT	AGAAGAAAAC	2340

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100	ACCCCTTATTG ATGGGAATGT ATGTGCCAAA AATATTCTGC TTATCAGAGA AGAAGACAGG	2400
101	AAGACAGGAA ATCCTCCCTT CATCAAACCTT AGTGATCCTG GCATTAGTAT TACAGTTTG	2460
102	CCAAAGGACA TTCTTCAGGA GAGAATACCA TGGGTACCACT CTGAATGCAT TGAAAATCCT	2520
103	AAAAATTAA ATTTGGCAAC AGACAAATGG AGTTTTGGTA CCACTTGTG GGAAATCTGC	2580
104	AGTGGAGGAG ATAAACCTCT AAGTGCTCTG GATTCTAAA GAAAGCTACA ATTTTATGAA	2640
105	GATAGGCATC AGCTTCCTGC ACCAAAGTGG GCAGAATTAG CAAACCTTAT AAATAATTGT	2700
106	ATGGATTATG AACCAAGATT CAGGCCTTCT TTCAGAGCCA TCATACGAGA TCTTAACAGT	2760
107	TTGTTTACTC CAGATTATGA ACTATTAACA GAAAATGACA TGTTACAAA TATGAGGATA	2820
108	GGTGCCTTGG GGTTTCTGG TGCCCTTGAA GACCGGGATC CTACACAGTT TGAAGAGAGA	2880
109	CATTGAAAT TTCTACAGCA ACTTGGCAAG GGTAAATTG GGAGTGTGGA GATGTGCCGG	2940
110	TATGACCCCTC TACAGGACAA CACTGGGGAG GTGGTCGCTG TAAAAAAAGCT TCAGCATAGT	3000
111	ACTGAAGAGC ACCTAAGAGA CTTTGAAAGG GAAATTGAAA TCCTGAAATC CCTACAGCAT	3060
112	GACAACATTG TAAAGTACAA GGGAGTGTGC TACAGTGCTG GTCGGCGTAA TCTAAAATTA	3120
113	ATTATGGAAT ATTTACCACT TGGAAGTTTA CGAGACTATC TTCAAAAACA TAAAGAACGG	3180
114	ATAGATCACA TAAAACCTCT GCAGTACACA TCTCAGATAT GCAAGGGTAT GGAGTATCTT	3240
115	GGTACAAAAA GGTATATCCA CAGGGATCTG GCAACGAGAA ATATATTGGT GGAGAACGAG	3300
116	AACAGAGTTA AAATTGGRGA TTTTGGGTTA ACCAAAGTCT TGCCACAAGA CAAAGAACATC	3360
117	TATAAAGTAA AAGAACCTGG TGAAAGTCCC ATATTCTGGT ATGCTCCAGA ATCACTGACA	3420
118	GAGAGCAAGT TTTCTGTGGC CTCAGATGTT TGGAGCTTG GAGTGGTTCT GTATGAACCTT	3480
119	TTCACATACA TTGAGAAGAG TAAAAGTCCA CCAGCGGAAT TTATGCGTAT GATTGGCAAT	3540
120	GACAAACAAG GACAGATGAT CGTGTCCAT TTGATAGAAC TTTGAAGAA TAATGGAAGA	3600
121	TTACCAAGAC CAGATGGATG CCCAGATGAG ATCTATATGA TCATGACAGA ATGCTGGAAC	3660
122	AATAATGTA ATCAACGCC CTCCTTTAGG GATCTAGCTC TTCGAGTGGA TCAAATAAGG	3720
123	GATAACATGG CTGGATGAAA GAAATGACCT TCATTCTGAG ACCAAAGTAG ATTTACAGAA	3780
124	CAAAGTTTA TATTCACAT TGCTGTGGAC TATTATTACA TATATCATTAA TTATATAAAT	3840
125	CATGATGCTA GCCAGCAAAG ATGTGAAAAT ATCTGCTCAA AACTTTCAAA GTTTAGTAAG	3900
126	TTTTCTTCA TGAGGCCACC AGTAAAAGAC ATTAATGAGA ATTCCTTAGC AAGGATTTG	3960
127	TAAGAAGTTT CTTAACACATT GTCAAGTTAAC ATCACTCTG TCTGGCAAAA GAAAAAAAT	4020
128	AGACTTTTC AACTCAGCTT TTTGAGACCT GAAARAATTAA TTATGTAAT TTTGCAATGT	4080
129	TAAAGATGCA CAGAATATGT ATGTATAGTT TTTACCACAG TGGATGTATA ATACCTTGGC	4140
130	ATCTTGTGTG ATGTTTAACA CACATGAGGG CTGGTGTCA TTAATACTGT TTTCTAATTT	4200
131	TTCCATGGTT AATCTATAAT TAATTACTTC ACTAAACAAA CAAATTAAGA TGTTCAGATA	4260
132	ATTGAATAAG TACCTTTGTG TCCTGTTCA TTTATATCGC TGGCCAGCAT TATAAGCAGG	4320
133	TGTATACTTT TAGCTTGAG TTCCATGTAC TGTAAATATT TTTCACATAA AGGGAACACAA	4380
134	TGTCTAGTTT TATTTGTATA GGAAATTGTC CCTGACCCCTA AATAATACAT TTTGAAATGA	4440
135	AAACAGCTTA AAAAAAAA AAAAAAAA AAAAAAAA AG	4482

136
137 (2) INFORMATION FOR SEQ ID NO:2:

138
139 (i) SEQUENCE CHARACTERISTICS:
140 (A) LENGTH: 1132 amino acids
141 (B) TYPE: amino acid
142 (C) STRANDEDNESS: single
143 (D) TOPOLOGY: linear

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145 (ii) MOLECULE TYPE: peptide

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147 (vii) IMMEDIATE SOURCE:
148 (A) LIBRARY:
149 (B) CLONE:

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152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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153 Met Gly Met Ala Cys Leu Thr Met Thr Glu Met Glu Gly Thr Ser Thr
 154 1 5 10 15
 155 Ser Ser Ile Tyr Gln Asn Gly Asp Ile Ser Gly Asn Ala Asn Ser Met
 156 20 25 30
 157 Lys Gln Ile Asp Pro Val Leu Gln Val Tyr Leu Tyr His Ser Leu Gly
 158 35 40 45
 159 Lys Ser Glu Ala Asp Tyr Leu Thr Phe Pro Ser Gly Glu Tyr Val Gly
 160 50 55 60
 161 Glu Glu Ile Cys Ile Ala Ala Ser Lys Ala Cys Gly Ile Thr Pro Val
 162 65 70 75 80
 163 Tyr His Asn Met Phe Ala Leu Met Ser Glu Thr Glu Arg Ile Trp Tyr
 164 85 90 95
 165 Pro Pro Asn His Val Phe His Ile Asp Glu Ser Thr Arg His Asn Val
 166 100 105 110
 167 Leu Tyr Arg Ile Arg Phe Tyr Phe Pro Arg Trp Tyr Cys Ser Gly Ser
 168 115 120 125
 169 Asn Arg Ala Tyr Arg His Gly Ile Ser Arg Gly Ala Glu Ala Pro Leu
 170 130 135 140
 171 Leu Asp Asp Phe Val Met Ser Tyr Leu Phe Ala Gln Trp Arg His Asp
 172 145 150 155 160
 173 Phe Val His Gly Trp Ile Lys Val Pro Val Thr His Glu Thr Gln Glu
 174 165 170 175
 175 Glu Cys Leu Gly Met Thr Val Leu Asp Met Met Arg Ile Ala Lys Glu
 176 180 185 190
 177 Asn Asp Gln Thr Pro Leu Ala Ile Tyr Asn Ser Ile Ser Tyr Lys Thr
 178 195 200 205
 179 Phe Leu Pro Gln Cys Ile Arg Ala Lys Ile Gln Asp Tyr His Ile Leu
 180 210 215 220
 181 Thr Arg Lys Arg Ile Arg Tyr Arg Phe Arg Arg Phe Ile Gln Gln Phe
 182 225 230 235 240
 183 Ser Gln Cys Lys Ala Thr Ala Arg Asn Leu Lys Leu Lys Tyr Leu Ile
 184 245 250 255
 185 Asn Leu Glu Thr Leu Gln Ser Ala Phe Tyr Thr Glu Lys Phe Glu Val
 186 260 265 270
 187 Lys Glu Pro Gly Ser Gly Pro Ser Gly Glu Glu Ile Phe Ala Thr Ile
 188 275 280 285
 189 Ile Ile Thr Gly Asn Gly Gly Ile Gln Trp Ser Arg Gly Lys His Lys
 190 290 295 300
 191 Glu Ser Glu Thr Leu Thr Glu Gln Asp Leu Gln Leu Tyr Cys Asp Phe
 192 305 310 315 320
 193 Pro Asn Ile Ile Asp Val Ser Ile Lys Gln Ala Asn Gln Glu Gly Ser
 194 325 330 335
 195 Asn Glu Ser Arg Val Val Thr Ile His Lys Gln Asp Gly Lys Asn Leu
 196 340 345 350
 197 Glu Ile Glu Leu Ser Ser Leu Arg Glu Ala Leu Ser Phe Val Ser Leu
 198 355 360 365
 199 Ile Asp Gly Tyr Tyr Arg Leu Thr Ala Asp Ala His His Tyr Leu Cys
 200 370 375 380
 201 Lys Glu Val Ala Pro Pro Ala Val Leu Glu Asn Ile Gln Ser Asn Cys
 202 385 390 395 400
 203 His Gly Pro Ile Ser Met Asp Phe Ala Ile Ser Lys Leu Lys Lys Ala
 204 405 410 415
 205

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206 Gly Asn Gln Thr Gly Leu Tyr Val Leu Arg Cys Ser Pro Lys Asp Phe
 207 420 425 430
 208 Asn Lys Tyr Phe Leu Thr Phe Ala Val Glu Arg Glu Asn Val Ile Glu
 209 435 440 445
 210 Tyr Lys His Cys Leu Ile Thr Lys Asn Glu Asn Glu Glu Tyr Asn Leu
 211 450 455 460
 212 Ser Gly Thr Lys Lys Asn Phe Ser Ser Leu Lys Asp Leu Leu Asn Cys
 213 465 470 475 480
 214 Tyr Gln Met Glu Thr Val Arg Ser Asp Asn Ile Ile Phe Gln Phe Thr
 215 485 490 495
 216 Lys Cys Cys Pro Pro Lys Pro Lys Asp Lys Ser Asn Leu Leu Val Phe
 217 500 505 510
 218 Arg Thr Asn Gly Val Ser Asp Val Pro Thr Ser Pro Thr Leu Gln Arg
 219 515 520 525
 220 Pro Thr His Met Asn Gln Met Val Phe His Lys Ile Arg Asn Glu Asp
 221 530 535 540
 222 Leu Ile Phe Asn Glu Ser Leu Gly Gln Gly Thr Phe Thr Lys Ile Phe
 223 545 550 555 560
 224 Lys Gly Val Arg Arg Glu Val Gly Asp Tyr Gly Gln Leu His Glu Thr
 225 565 570 575
 226 Glu Val Leu Leu Lys Val Leu Asp Lys Ala His Arg Asn Tyr Ser Glu
 227 580 585 590
 228 Ser Phe Phe Glu Ala Ala Ser Met Met Ser Lys Leu Ser His Lys His
 229 595 600 605
 230 Leu Val Leu Asn Tyr Gly Val Cys Val Cys Gly Asp Glu Asn Ile Leu
 231 610 615 620
 232 Val Gln Glu Phe Val Lys Phe Gly Ser Leu Asp Thr Tyr Leu Lys Lys
 233 625 630 635 640
 234 Asn Lys Asn Cys Ile Asn Ile Leu Trp Lys Leu Glu Val Ala Lys Gln
 235 645 650 655
 236 Leu Ala Trp Ala Met His Phe Leu Glu Glu Asn Thr Leu Ile His Gly
 237 660 665 670
 238 Asn Val Cys Ala Lys Asn Ile Leu Ile Arg Glu Glu Asp Arg Lys
 239 675 680 685
 240 Thr Gly Asn Pro Pro Phe Ile Lys Leu Ser Asp Pro Gly Ile Ser Ile
 241 690 695 700
 242 Thr Val Leu Pro Lys Asp Ile Leu Gln Glu Arg Ile Pro Trp Val Pro
 243 705 710 715 720
 244 Pro Glu Cys Ile Glu Asn Pro Lys Asn Leu Asn Leu Ala Thr Asp Lys
 245 725 730 735
 246 Trp Ser Phe Gly Thr Thr Leu Trp Glu Ile Cys Ser Gly Gly Asp Lys
 247 740 745 750
 248 Pro Leu Ser Ala Leu Asp Ser Gln Arg Lys Leu Gln Phe Tyr Glu Asp
 249 755 760 765
 250 Arg His Gln Leu Pro Ala Pro Lys Trp Ala Glu Leu Ala Asn Leu Ile
 251 770 775 780
 252 Asn Asn Cys Met Asp Tyr Glu Pro Asp Phe Arg Pro Ser Phe Arg Ala
 253 785 790 795 800
 254 Ile Ile Arg Asp Leu Asn Ser Leu Phe Thr Pro Asp Tyr Glu Leu Leu
 255 805 810 815
 256 Thr Glu Asn Asp Met Leu Pro Asn Met Arg Ile Gly Ala Leu Gly Phe
 257 820 825 830
 258 Ser Gly Ala Phe Glu Asp Arg Asp Pro Thr Gln Phe Glu Glu Arg His

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/467,100

DATE: 04/14/2000
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Line

Error

Original Text